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SEQUENCE LISTING

> University of California, San Francisco  
Farinas, Javier

<120> Methods and Reagents for Targeting Organic Compounds To Selected  
Cellular Locations

<130> UCSF1100-3

<140> 09/403,882

<141> 2000-03-20

<150> 60/081,340

<151> 1998-04-09

<150> 60/081,118

<151> 1998-04-08

<160> 9

<170> PatentIn version 3.0

<210> 1

<211> 951

<212> DNA

<213> artificial

<220>

<223> single chain antibody

<220>

<221> CDS

<222> (1)..(951)

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gga ggg tcc cgg aaa ctc tcc tgt gca gcc tct gga ttc act ttc agt 96  
Gly Gly Ser Arg Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser  
20 25 30

agc ttt gga atg cac tgg gtt cgt cag gct cca gag aag ggg ctg gag 144  
Ser Phe Gly Met His Trp Val Arg Gln Ala Pro Glu Lys Gly Leu Glu  
35 40 45

tgg gtc gca tat att agt agt ggc agt agt acc atc tac tat gca gac 192  
Trp Val Ala Tyr Ile Ser Ser Gly Ser Ser Thr Ile Tyr Tyr Ala Asp  
50 55 60

aca gtg aag gga cga ttc acc atc tcc aga gac aat ccc aag aac acc 240  
Thr Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Pro Lys Asn Thr  
65 70 75 80

ctg ttc ctg caa atg acc agt cta agg tct gag gac acg gtc atg tat 288  
Leu Phe Leu Gln Met Thr Ser Leu Arg Ser Glu Asp Thr Val Met Tyr  
85 90 95

tac tgt gca aga gat tac ggg gct tat tgg ggc caa ggg acc acg gtc 336

Tyr	Cys	Ala	Arg	Asp	Tyr	Gly	Ala	Tyr	Trp	Gly	Gln	Gly	Thr	Thr	Val		
			100					105					110				
acc	gtc	tcc	tca	ggg	gga	ggc	ggc	tca	ggc	gga	ggg	ggc	tct	ggc	ggg		384
Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly		
		115					120					125					
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ggc	gga	tcg	gac	att	gag	ctc	acc	cag	tct	cca	gca	atc	atg	tct	gca		432
Gly	Gly	Ser	Asp	Ile	Glu	Leu	Thr	Gln	Ser	Pro	Ala	Ile	Met	Ser	Ala		
		130				135					140						
tct	cca	ggg	gag	agg	gtc	acc	atg	acc	tgc	agt	gcc	agt	tca	agt	gta		480
Ser	Pro	Gly	Glu	Arg	Val	Thr	Met	Thr	Cys	Ser	Ala	Ser	Ser	Ser	Val		
145					150					155					160		
agg	tac	atg	aac	tgg	ttc	caa	cag	aag	tca	ggc	acc	tcc	ccc	aaa	aga		528
Arg	Tyr	Met	Asn	Trp	Phe	Gln	Gln	Lys	Ser	Gly	Thr	Ser	Pro	Lys	Arg		
			165					170						175			
tgg	att	tat	gac	aca	tcc	aaa	ctg	tct	tct	gga	gtc	cct	gct	cgc	ttc		576
Trp	Ile	Tyr	Asp	Thr	Ser	Lys	Leu	Ser	Ser	Gly	Val	Pro	Ala	Arg	Phe		
			180					185					190				
agt	ggc	agt	ggg	tct	ggg	acc	tct	tac	tct	ctc	aca	atc	agc	agc	atg		624
Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile	Ser	Ser	Met		
		195					200					205					
gag	gct	gaa	gat	gct	gcc	act	tac	tac	tgc	cag	cag	tgg	agt	agt	aac		672
Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp	Ser	Ser	Asn		
	210				215					220							
cca	ctc	acg	ttc	ggg	gct	ggg	acc	aag	ctg	gag	ctg	aaa	cgg	gcg	gcc		720
Pro	Leu	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Leu	Lys	Arg	Ala	Ala		
225					230					235					240		
gca	gaa	caa	aaa	ctc	atc	tca	gaa	gag	gat	ctg	aat	ggg	gcc	gtc	gac		768
Ala	Glu	Gln	Lys	Leu	Ile	Ser	Glu	Glu	Asp	Leu	Asn	Gly	Ala	Val	Asp		
				245					250					255			
gaa	caa	aaa	ctc	atc	tca	gaa	gag	gat	ctg	aat	gct	gtg	ggc	cag	gac		816
Glu	Gln	Lys	Leu	Ile	Ser	Glu	Glu	Asp	Leu	Asn	Ala	Val	Gly	Gln	Asp		
			260					265					270				
acg	cag	gag	gtc	atc	gtg	gtg	cca	cac	tcc	ttg	ccc	ttt	aag	gtg	gtg		864
Thr	Gln	Glu	Val	Ile	Val	Val	Pro	His	Ser	Leu	Pro	Phe	Lys	Val	Val		
		275					280					285					
gtg	atc	tca	gcc	atc	ctg	gcc	ctg	gtg	gtg	ctc	acc	atc	atc	tcc	ctt		912
Val	Ile	Ser	Ala	Ile	Leu	Ala	Leu	Val	Val	Leu	Thr	Ile	Ile	Ser	Leu		
	290				295					300							
atc	atc	ctc	atc	atg	ctt	tgg	cag	aag	aag	cca	cgt	tag					951
Ile	Ile	Leu	Ile	Met	Leu	Trp	Gln	Lys	Lys	Pro	Arg						
305					310					315							

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Met Ala Glu Val Lys Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro  
 1 5 10 15

Gly Gly Ser Arg Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser  
 20 25 30

Ser Phe Gly Met His Trp Val Arg Gln Ala Pro Glu Lys Gly Leu Glu  
 35 40 45

Trp Val Ala Tyr Ile Ser Ser Gly Ser Ser Thr Ile Tyr Tyr Ala Asp  
 50 55 60

Thr Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Pro Lys Asn Thr  
 65 70 75 80

Leu Phe Leu Gln Met Thr Ser Leu Arg Ser Glu Asp Thr Val Met Tyr  
 85 90 95

Tyr Cys Ala Arg Asp Tyr Gly Ala Tyr Trp Gly Gln Gly Thr Thr Val  
 100 105 110

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly  
 115 120 125

Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser Pro Ala Ile Met Ser Ala  
 130 135 140

Ser Pro Gly Glu Arg Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val  
 145 150 155 160

Arg Tyr Met Asn Trp Phe Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg  
 165 170 175

Trp Ile Tyr Asp Thr Ser Lys Leu Ser Ser Gly Val Pro Ala Arg Phe  
 180 185 190

Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met  
 195 200 205

Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn  
 210 215 220

Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Ala Ala  
 225 230 235 240

Ala Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Val Asp  
                   245                  250                  255

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ala Val Gly Gln Asp  
                   260                  265                  270

Thr Gln Glu Val Ile Val Val Pro His Ser Leu Pro Phe Lys Val Val  
                   275                  280                  285

Val Ile Ser Ala Ile Leu Ala Leu Val Val Leu Thr Ile Ile Ser Leu  
                   290                  295                  300

Ile Ile Leu Ile Met Leu Trp Gln Lys Lys Pro Arg  
                   305                  310                  315

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<220>  
 <223> antisense primer containing Xba I site

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 gctctagact ggcccacagc attcagatcc tc

32

<210> 4  
 <211> 28  
 <212> DNA  
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<220>  
 <223> sense primer containing EcoR1

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28

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 <223> localization sequence targeting the nucleus

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Lys Lys Lys Arg Lys  
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<223> localization sequence targeting the mitochondrion

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Met Leu Arg Thr Ser Ser Leu Phe Thr Arg Arg Val Gln Pro Ser Leu  
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Phe Arg Asn Ile Leu Arg Leu Gln Ser Thr  
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Lys Asp Glu Leu  
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<210> 8

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<223> insertion into plasma membrane

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<221> VARIANT

<222> (1)..(4)

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Cys Cys Xaa Xaa  
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<211> 6

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<220>

<223> specific targeting sequences c-terminal

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Ser Glu Lys Asp Glu Leu  
1 5